

What Is Claimed Is:

1. An isolated polypeptide comprising the amino acid sequence SEQ ID NO:2.
2. A method of producing lysine comprising culturing the host cells of a vector comprising an isolated polynucleotide molecule comprising a nucleotide sequence encoding the polypeptide sequence of SEQ ID NO:2, wherein said host cells comprise one or more of:
 - (a) increased enzyme activity of one or more lysine biosynthetic pathway enzymes compared to the genetically unaltered host cell;
 - (b) one or more copies of each gene encoding a lysine biosynthetic pathway enzyme; and
 - (c) alteration of one or more transcription factors regulating transcription of one or more genes encoding a lysine biosynthetic pathway enzyme, wherein said host cell produces lysine in said culture medium
3. The method of claim 2 wherein said increased enzyme activity comprises overexpressing one or more genes encoding one or more lysine biosynthetic pathway enzymes.
4. The method of claim 3 wherein said one or more genes are operably linked directly or indirectly to one or more promoter sequences.
5. The method of claim 4 wherein said operably linked promoter sequences are heterologous, endogenous, or hybrid.
6. The method of claim 5 wherein said promoter sequences are one or more of a promoter sequence from the 5' end of genes endogenous to *C. glutamicum*, a promoter sequence from plasmids that replicate in *C. glutamicum*, and, a promoter sequence from the genome of phage which infect *C. glutamicum*.
7. The method of claim 5 or 6 wherein one or more of said promoter sequences are modified.
8. The method of claim 7 wherein said modification comprises truncation at the 5' end, truncation at the 3' end, non-terminal insertion of one or more

nucleotides, non-terminal deletion of one or more nucleotides, addition of one or more nucleotides at the 5' end, addition of one or more nucleotides at the 3' end, and, combinations thereof.

9. The method of claim 2 wherein said increased enzyme activity results from the activity of one or more modified lysine biosynthetic pathway enzymes wherein said enzyme modification results in a change in kinetic parameters, allosteric regulation, or both, compared to the enzyme lacking said modification.

10. The method of claim 9 wherein said change in kinetic parameters is a change in K_m , V_{max} or both.

11. The method of claim 9 wherein said change in allosteric regulation is a change in one or more enzyme allosteric regulatory sites.

12. The method of claim 9 wherein said modification is a result of a change in the nucleotide sequence encoding said enzyme.

13. The method of claim 12 wherein said change in said nucleotide sequence is an addition, insertion, deletion, substitution, or a combination thereof, of one or more nucleotides.

14. The method of claim 2 wherein said alteration of one or more transcription factors comprises one or more mutations in transcription inhibitor proteins, one or more mutations in transcription activator proteins, or both, wherein said one or more mutations increases transcription of the target nucleotide sequence compared to the transcription by said one or more transcription factors lacking said alteration.

15. The method of claim 14 wherein said one or more mutations is a change in said nucleotide sequence encoding said transcription factor.

16. The method of claim 15 wherein said change in said nucleotide sequence is an addition, insertion, deletion, substitution, or a combination thereof, of one or more nucleotides.

17. An isolated polypeptide wherein said polypeptide comprises an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO: 19.

18. The polypeptide of claim 17 wherein said polypeptide has the amino acid sequence of SEQ ID NO: 19.
19. An isolated polynucleotide molecule comprising a nucleotide sequence encoding the polypeptide of claim 17.
20. The isolated polynucleotide molecule of claim 19 comprising a nucleic acid having the sequence of SEQ ID NO: 18.
21. A vector comprising the polynucleotide molecule of claim 19.
22. A host cell comprising the vector of claim 21.
23. The host cell of claim 22 wherein said host cell is NRRL B30360.
24. A method for selecting a transformed host cell comprising:
 - (a) transforming a *Corynebacterium* species host cell with the polynucleotide molecule of claim 19, and
 - (b) selecting a transformed host cell.
25. An isolated polypeptide wherein said polypeptide comprises a polypeptide having at least 95% sequence identity to the amino acid sequence of SEQ ID NO:21.
26. The polypeptide of claim 25 having the amino acid sequence of SEQ ID NO: 21.
27. An isolated polynucleotide molecule comprising a nucleotide sequence encoding the polypeptide of claim 25.
28. The isolated polynucleotide molecule of claim 27 comprising a nucleic acid having the sequence of SEQ ID NO: 20.
29. A vector comprising the polynucleotide molecule of claim 27.
30. A host cell comprising the vector of claim 29.
31. The host cell of claim 30 wherein said host cell is selected from the group consisting of NRRL B30218, NRRL B30220 and NRRL B30222.
32. A method for selecting a transformed host cell comprising:
 - (a) transforming a *Corynebacterium* species host cell with the polynucleotide molecule of claim 27, and
 - (b) selecting a transformed host cell.